Amendments to the Specification

Please replace the first full paragraph on page 19 (beginning at line 7) with the following paragraph:

The expression pattern of [[OE]]BM-HABP was also examined in human smooth muscle cells (SMC's), human fetal lung fibroblasts (ETL), human umbilical vein endothelial cells (HUVECs), as well as in HL-60 and U937 cells. There was no detectable mRNA expression of BM-HABP in any of the above cell lines.

Please replace the second full paragraph on page 20 (beginning at line 21) with the following paragraph:

The determined nucleotide sequence of the BM-HABP cDNA of Figures 4A-B (SEQ ID NO:10) contains an open reading frame encoding a polytopic polypeptide of about 353 amino acid residues, with a HA-binding domain, 6 transmembrane domains, 4 extracellular domains, and a pore loop, and having a deduced molecular weight of about 36063.32 Da. The BM-HABP protein shown in Figures 4A-B (SEQ ID NO:11) is predicted to be about 43% identical across amino acids 52 to 155 to the TSG-6 protein depicted in SEQ ID NO:12 (approximately 31% identical overall, see Figure 8) using the computer program "MegAlign" (DNAstar suite of software programs). In addition to having homology, the TSG-6 protein and BM-HABP are thought to share the same topological structure based upon their intrinsic hyaluronan binding activity. For example, like the TSG-6 protein, BM-HABP contains a hyaluronan binding domain. As discussed above, TSG-6 protein has been shown to be a hyaluronan binding protein and play a vital role in arthritis, anti-inflammatory activity, and the vascular injury response.

Please amend the last paragraph on page 34, which continues onto page 35 as follows:

In another embodiment, the full-length WF-HABP invention provides isolated nucleic acid molecules comprising polynucleotides which hybridize, preferably under stringent hybridization conditions, to a portion of one or more of the nucleic acids (i.e.,

polynucleotides) described herein, such as, for instance, the cDNA clone contained in ATCC Deposit 203503, the polynucleotide sequence depicted in Figures 1A-H (SEQ ID NO:1) or the complementary strand thereto, and/or any of the polynucleotide fragments as described herein. By "stringent hybridization conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (~~150~~ 750 mM NaCl, ~~15~~ 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C. By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least 15 nucleotides (nt), and more preferably at least 20 nt, still more preferably at least 30 nt, and even more preferably 30-70, or 80-150 nt, or the entire length of the reference polynucleotide. By a portion of a polynucleotide of "at least 20 nt in length," for example, is intended 20 or more contiguous nucleotides from the nucleotide sequence of the reference polynucleotide (e.g., the complementary strand of the nucleotide sequence shown in Figures 1A-H (SEQ ID NO:1)). Of course, a polynucleotide which hybridizes only to a poly A sequence (such as the 3' terminal poly(A) tail of a cDNA sequence), or to a complementary stretch of T (or U) residues, would not be included in a polynucleotide of the invention used to hybridize to a portion of a nucleic acid of the invention, since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (i.e., practically any double-stranded cDNA clone generated using oligo dT as a primer). These polynucleotides have uses which include, but are not limited to, diagnostic probes and primers as discussed above and in more detail below.